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A new species of *Cyrtodactylus* Gray, 1827 (Squamata, Gekkonidae) from Yunnan, China

Shuo Liu[1], Dingqi Rao[2]

1 *Kunming Natural History Museum of Zoology, Kunming Institute of Zoology, Chinese Academy of Sciences, 32 Jiaochang Donglu, Kunming, Yunnan 650223, China* **2** *Kunming Institute of Zoology, Chinese Academy of Sciences, 32 Jiaochang Donglu, Kunming, Yunnan 650223, China*

Corresponding authors: Dingqi Rao (raodq@mail.kiz.ac.cn); Shuo Liu (liushuo@mail.kiz.ac.cn)

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Abstract

A new species of *Cyrtodactylus* is described on the basis of five specimens collected from the karst formations of Zhenkang County, Yunnan Province, China. *Cyrtodactylus zhenkangensis* **sp. nov.** is recognized by having a unique combination of morphological characters, the most diagnostic being: 12–15 enlarged femoral scales on each thigh; 2–5 femoral pores on each thigh in males, 0–3 pitted scales on each thigh in females; eight or nine precloacal pores in a continuous row or separated by one poreless scale in males, 7–9 pitted scales in females; subcaudals enlarged, arranged alternately as single and double on anterior and mostly single at middle and posterior; dorsal surface of head with obvious reticulations. Phylogenetic analyses show that the new species is a member of the *C. wayakonei* species group and a sister taxon to a clade consisting of *C. wayakonei* and *C. martini* based on Maximum Likelihood analyses and Bayesian Inference and differs from its congeners by at least 12.0% genetic divergence in a fragment of the COI gene.

Keywords

Bent-toed gecko, *Cyrtodactylus wayakonei*, karst-dwelling, taxonomy, Zhenkang

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Introduction

Bent-toed geckos of the genus *Cyrtodactylus* are one of the most species-diverse genera of gekkonid lizards (Kluge 2001; Uetz 2020), and many of these species are thought to be highly localized with extremely narrow geographic ranges (Nazarov et al. 2012; Luu et al. 2016; Grismer et al. 2018, 2020; Murdoch et al. 2019). At present, the genus contains more than 300 recognized species (Uetz et al. 2020), and approximately 150 new species have been described since 2010 and most of these new discoveries were from Southeast Asia (Schneider et al. 2020).

During our recent fieldwork in Yunnan Province, China, a series of bent-toed geckos was collected from the karst formations of Zhenkang County. Morphological and molecular phylogenetic analyses revealed that the new collection belonged to an unnamed species of *Cyrtodactylus*. We describe it as a new species.

Materials and methods

Sampling

Fieldwork was conducted at night. Specimens were collected by hand. Photographs were taken to document color pattern in life prior to euthanization. Liver tissues were stored in 99% ethanol and specimens were preserved in 75% ethanol. Specimens were deposited at Kunming Natural History Museum of Zoology, Kunming Institute of Zoology, Chinese Academy of Sciences (**KIZ**).

Molecular analyses

Molecular data were generated for three specimens and analyzed with the available homologous sequences of the *Cyrtodactylus wayakonei* species group obtained from GenBank. The new sequences were deposited in GenBank under accession numbers MW593136–MW593138. Sequences of *C.* cf. *interdigitalis* Ulber, 1993 and *C. elok* Dring, 1979 were used as outgroups according to Nguyen et al. (2017) and Schneider et al. (2020).

We used the protocols of Le et al. (2006) for DNA extraction, amplification, and sequencing. DNA extraction used the standard three-step phenol/trichloromethane protocol (Sambrook et al. 1989). A fragment of the mitochondrial gene, cytochrome c oxidase subunit 1 (COI) was amplified in a volume consisted of 25 µl (10 µl of mastermix, 5 µl of water, 2 µl of each primer at 10 pmol/µl and 6 µl of DNA) by the polymerase chain reaction (PCR; 35 cycles of 95 °C for 30 s, 53 °C for 40 s, 72 °C for 90 s) and sequenced using the primer pair VF1-d (TTCTCAACCAACCACAARGAYATYGG) and VR1-d (TAGACTTCTGGGTGGCCRAARAAYCA) (Ivanova et al. 2006). PCR products were cleaned using ExoSAP-IT (Applied Biosystems) and sequenced in both directions by direct double strand cycle sequencing using the BigDye Terminator v. 3.1 Cycle Sequencing Kit on a

3130 DNA Analyzer (Applied Biosystems). Sequences were edited with Sequencher v. 5.4.6 (Gene Codes).

Sequences were aligned using ClustalW (Thompson et al. 1994) integrated in MEGA v. 7 (Kumar et al. 2016) with default parameters. Pairwise distances between species were calculated in MEGA v. 7 with the parameters Transitions + Transversions, Uniform rates, and Pairwise deletion (Kumar et al. 2016). The substitution model GTR+G+I was selected using the corrected Akaike Information Criterion (AICc) in MODELTEST v. 3.7 (Posada and Crandall 1998). Bayesian inference (BI) was performed in MrBayes v. 3.2.6 (Ronquist et al. 2012) based on the selected substitution model. Two runs were performed simultaneously with four Markov chains starting from random tree. The chains were run for 10,000,000 generations and sampled every 1000 generations. The first 25% of the sampled trees was discarded as burn-in after the standard deviation of split frequencies of the two runs reached a value of less than 0.01, and then the remaining trees were used to create a 50% majority-rule consensus tree and to estimate Bayesian posterior probabilities (BPP). Nodes with BPP of 95 and above were considered strongly supported (Huelsenbeck et al. 2001; Wilcox et al. 2002; Alfaro et al. 2003) and nodes with values of 90–94 as well supported (Chomdej et al. 2020). Maximum Likelihood (ML) analysis was performed in RaxmlGUI v. 1.5 (Silvestro and Michalak 2012), and nodal support was estimated by 1,000 rapid bootstrap replicates. Nodes with bootstrap values of 70 and above were considered significantly supported (Alfaro et al. 2003; Sitnikova 1996).

Morphological analyses

Measurements were taken with digital calipers to the nearest 0.1 mm. Bilateral scale counts were given as left/right. The methodology of measurements and meristic counts followed Ngo (2011) and Schneider et al. (2020):

AG axilla to groin distance;
DTR dorsal tubercle rows, number of dorsal, longitudinal rows of tubercles at midbody between the ventrolateral folds;
ED ear diameter, greatest diameter of ear;
EE eye orbit to ear distance, from posterior corner of eye orbit to anterior margin of ear opening;
EFS enlarged femoral scales, number of enlarged femoral scale beneath each thigh;
ForeaL forearm length, from the base of the palm to the elbow;
FP femoral pores;
GSDT granular scales surrounding dorsal midbody tubercles;
HH maximum head height, from occiput to underside of jaws;
HL head length, from tip of snout to posterior margin of ear;
HW maximum head width;
I postrostrals or internasals;
IFL infralabials;
IND internarial distance, measured between inner borders of nostrils;

IOD interorbital distance, measured across narrowest point of frontal bone;
LD4 subdigital lamellae under the fourth finger;
LT4 subdigital lamellae under the fourth toe;
ML mental length;
MW mental width;
OD greatest diameter of orbit;
PAT postcloacal tubercles, number of tubercles on each side of postcloacal region;
PM postmentals, i.e. scales bordering mental shield, except infralabials;
PP precloacal pores;
PVT paravertebral tubercles, counted in a single paravertebral row from the level of the forelimb insertions to the level of the hind limb insertion;
RH rostral heigth;
RW rostral width;
SC5SPL scale rows between fifth supralabials;
SE snout to eye distance, from tip of snout to anterior corner of eye orbit;
SL shank length, from the base of heel to the knee;
SPL supralabials;
SVL snout-vent length, from tip of snout to anterior margin of cloaca;
TaL tail length, from posterior margin of cloaca to tip of tail;
V longitudinal ventral scale rows, counted across the belly between the ventrolateral folds at midbody.

Morphological comparisons and analyses were based on specimen examination and data obtained from the literature (Hoang et al. 2007; Rösler et al. 2008; Bauer et al. 2009, 2010; Ngo and Grismer 2010; Nguyen et al. 2010, 2015, 2017; Sumontha et al. 2010; Teynié and David 2010; Luu et al. 2011, 2013, 2016; Ngo 2011; Ngo and Chan 2011; Schneider et al. 2011, 2014, 2020; Kunya et al. 2014; Nazarov et al. 2014, 2018; Nguyen et al. 2014; Le 2016; Pham et al. 2019).

Results

Molecular analyses

The obtained sequence alignment is 690 bp in length. The topologies derived from ML and BI analyses were similar and basically consistent with those of Nguyen et al. (2017), Pham et al. (2019), and Schneider et al. (2020). The sequences of three specimens collected from Zhenkang County, Yunnan, China were nested them within the *Cyrtodactylus wayakonei* group and the sister group to a clade consisting of *C. wayakonei* Nguyen, Kingsada, Rösler, Auer & Ziegler, 2010 and *C. martini* Ngo, 2011 with strong support in ML and moderate support in BI (Fig. 1). The interspecific uncorrected genetic *p*-distances between the newly collected specimens and other members of *C. wayakonei* group ranged from 12.0% to 17.8% (Table 1).

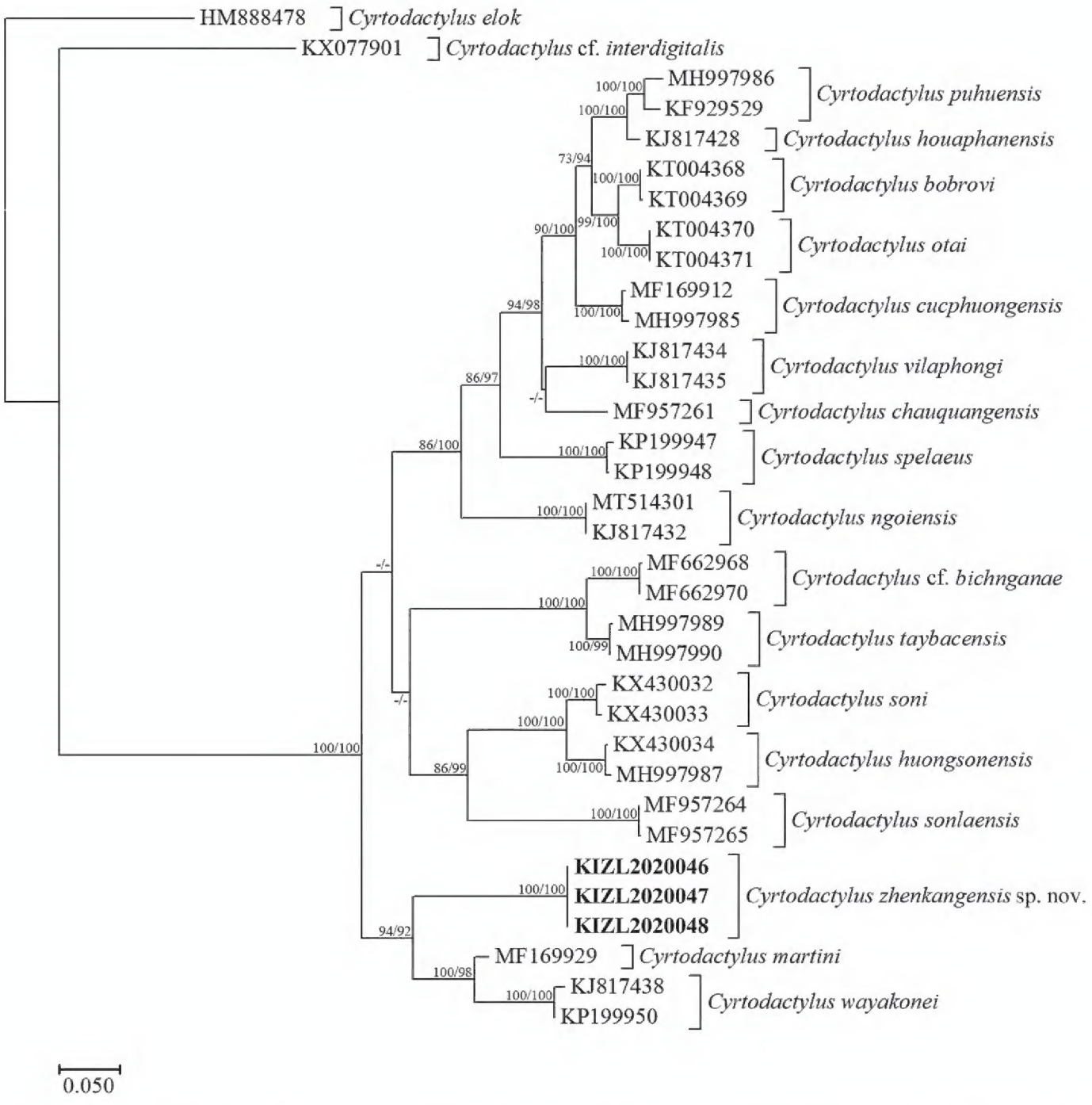

Figure 1. Bayesian Inference phylogram inferred from partial COI genes. Numbers before slashes indicate bootstrap support for Maximum Likelihood analyses and numbers after slashes indicate Bayesian posterior probabilities. The symbol "–" represents the value below 60.

Taxonomic accounts

***Cyrtodactylus zhenkangensis* sp. nov.**
http://zoobank.org/1CAE09BE-E522-42EF-AD5A-0E3B7A694CDB
Figs 2–5

Holotype. KIZL2020049, adult male, China, Yunnan Province, Lincang City, Zhenkang County, Nansan town, 23°46'32"N, 98°50'28"E, 1060 m elevation, collected on 11 September 2020 by Shuo Liu.

Paratypes. KIZL2020048 and KIZL2020050, two adult females; KIZL2020046, subadult male; and KIZL2020047, subadult female; all the same collection data as the holotype.

Table 1. Mean uncorrected pairwise genetic distances (%) based on 690 base pairs of COI gene sequences.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	*Cyrtodactylus bichnganae*																		
2	*C. bobrovi*	17.2																	
3	*C. chauquangensis*	15.3	9.3																
4	*C. cucphuongensis*	16.6	6.9	8.0															
5	*C. houaphanensis*	17.3	6.2	8.8	7.2														
6	*C. huongsonensis*	14.7	15.8	14.5	14.9	16.0													
7	*C. martini*	15.6	15.1	13.7	14.1	15.6	15.0												
8	*C. ngoiensis*	15.9	12.3	11.6	13.8	13.1	14.1	14.7											
9	*C. otai*	16.7	3.8	9.3	7.2	6.2	15.4	15.9	13.1										
10	*C. puhuensis*	18.8	7.2	10.3	8.2	3.4	17.7	16.1	15.0	7.3									
11	*C. soni*	13.6	16.7	14.5	15.8	16.4	5.3	15.4	15.0	16.3	18.7								
12	*C. sonlaensis*	15.4	16.3	16.8	16.7	17.7	13.4	14.6	15.4	17.3	18.8	14.0							
13	*C. spelaeus*	16.9	10.0	11.7	12.1	10.9	16.7	15.0	13.5	11.2	11.8	15.8	15.7						
14	*C. taybacensis*	5.2	16.1	14.4	15.4	16.2	15.1	14.7	15.6	16.4	17.5	14.4	16.1	15.3					
15	*C. vilaphongi*	16.4	9.3	8.2	9.5	8.2	15.3	14.7	12.9	9.4	10.1	15.9	17.1	11.8	15.9				
16	*C. wayakonei*	15.2	16.7	15.2	16.5	17.4	16.7	6.5	15.5	18.3	18.1	17.5	15.9	16.2	15.6	16.0			
17	*Cyrtodactylus zhenkangensis* sp. nov.	**17.8**	**15.0**	**14.9**	**15.8**	**16.2**	**16.7**	**12.0**	**14.3**	**16.1**	**16.8**	**17.1**	**17.1**	**15.7**	**16.8**	**16.4**	**13.1**		
18	*C. interdigitalis*	18.5	19.9	19.2	19.3	20.2	20.2	18.2	20.1	20.1	21.9	19.9	20.5	20.4	18.3	19.3	18.3	**19.9**	
19	*C. elok*	18.8	19.4	18.9	17.9	19.5	19.6	17.1	19.5	19.6	20.2	20.2	19.7	18.6	18.6	19.2	18.6	**19.5**	15.8

Etymology. The name refers to Zhenkang County, where the new species was found.

Diagnosis. *Cyrtodactylus zhenkangensis* sp. nov. differs from all other congeners by the following combination of characters: medium size (SVL 78.1–87.4 mm); ventrolateral folds present with interspersed tubercles; 12–15 enlarged femoral scales on each thigh; 2–5 femoral pores on each thigh in males, 0–3 pitted scales on each thigh in females; eight or nine precloacal pores in a continuous row or separated by one poreless scale in males, 7–9 pitted scales in females; two or three postcloacal tubercles on each side; 18–21 lamellae under finger IV, 21–23 lamellae under toe IV; subcaudals enlarged, arranged alternately as single and double on anterior and mostly single at middle and posterior; dorsal surface of head with obvious, light-colored reticulations; eight or nine irregular transverse bands on the dorsum of body.

Description of holotype. Adult male, SVL 87.4 mm; head distinguished from neck, moderately long (HL/SVL 0.27), relatively widened (HW/HL 0.79), slightly depressed (HH/HL 0.48); two supranasals separated by one internasal; nares oval, surrounded by supranasal, rostral, first supralabial, and three or four postnasals; loreal region concave; snout long (SE/HL 0.41), round anteriorly, longer than diameter of orbit (OD/SE 0.70); snout scales small, round, granular, larger than those in frontal and parietal regions; eye large (OD/HL 0.28), pupils vertical; upper eyelid fringe with spinous scales; ear opening oval, obliquely directed, small in size (ED/HL 0.08); rostral wider than high (RH/RW 0.66), medially divided dorsally by a suture, reaching to approximately half-way down rostral, in contact with first supralabial and nostrils laterally, and supranasals and internasal dorsally; mental triangular, narrower than rostral

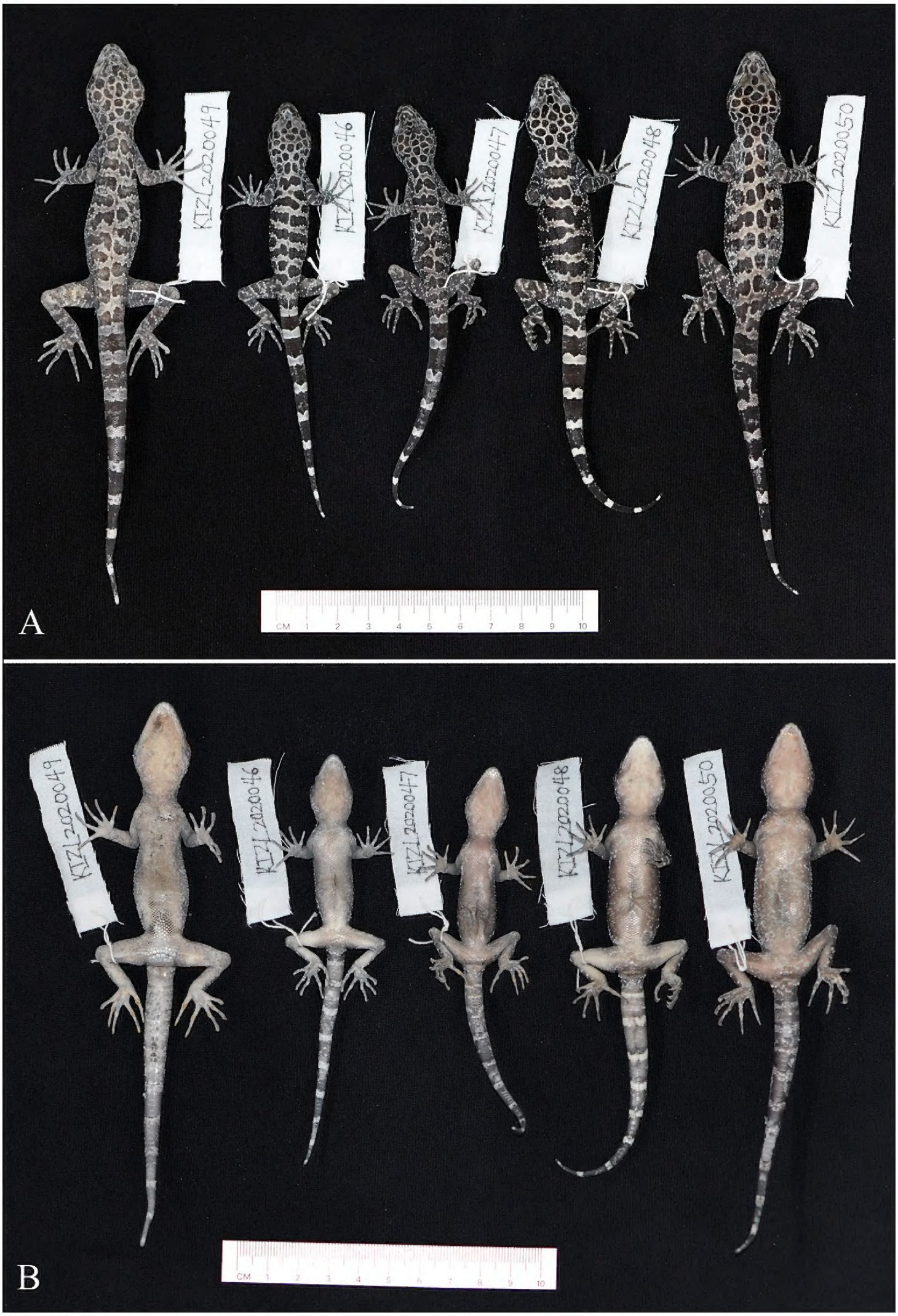

Figure 2. Type series of *Cyrtodactylus zhenkangensis* sp. nov. in preservative **A** dorsal view **B** ventral view.

Figure 3. Close-up views of the holotype (KIZL20200049) of *Cyrtodactylus zhenkangensis* sp. nov. in preservative **A** dorsal view of head **B** ventral view of head **C** right side femoral region **D** precloacal region **E** left side femoral region **F** subcaudal scales.

(MW/RW 0.83), wider than high (ML/MW 0.82); two postmentals, enlarged, in contact posteriorly, bordered by mental anteromedially, first infralabial anterolaterally, and an enlarged chin scale posterolaterally; 10/10 supralabials; 10/10 infralabials.

Body slender (AG/SVL 0.41), ventrolateral folds slightly developed with interspersed tubercles; dorsal scales granular; dorsal tubercles round and weakly keeled, four or five times larger than the size of adjoining scales, conical, present on occiput, back and tail base, each surrounded by nine or ten granular scales, in 24 irregular longitudinal rows at the midbody, 29 paravertebral tubercles; ventral scales smooth, larger than those of dorsum, round, subimbricate, largest posteriorly, in 33 longitudinal rows at midbody; gular region with homogenous smooth scales; precloacal groove absent; three rows of enlarged scales present in posterior region of pore-bearing scales; 13/15 enlarged femoral scales beneath thighs continuous with enlarged precloacal scales; femoral pores bearing scales separated from pore-bearing precloacal scales by six poreless

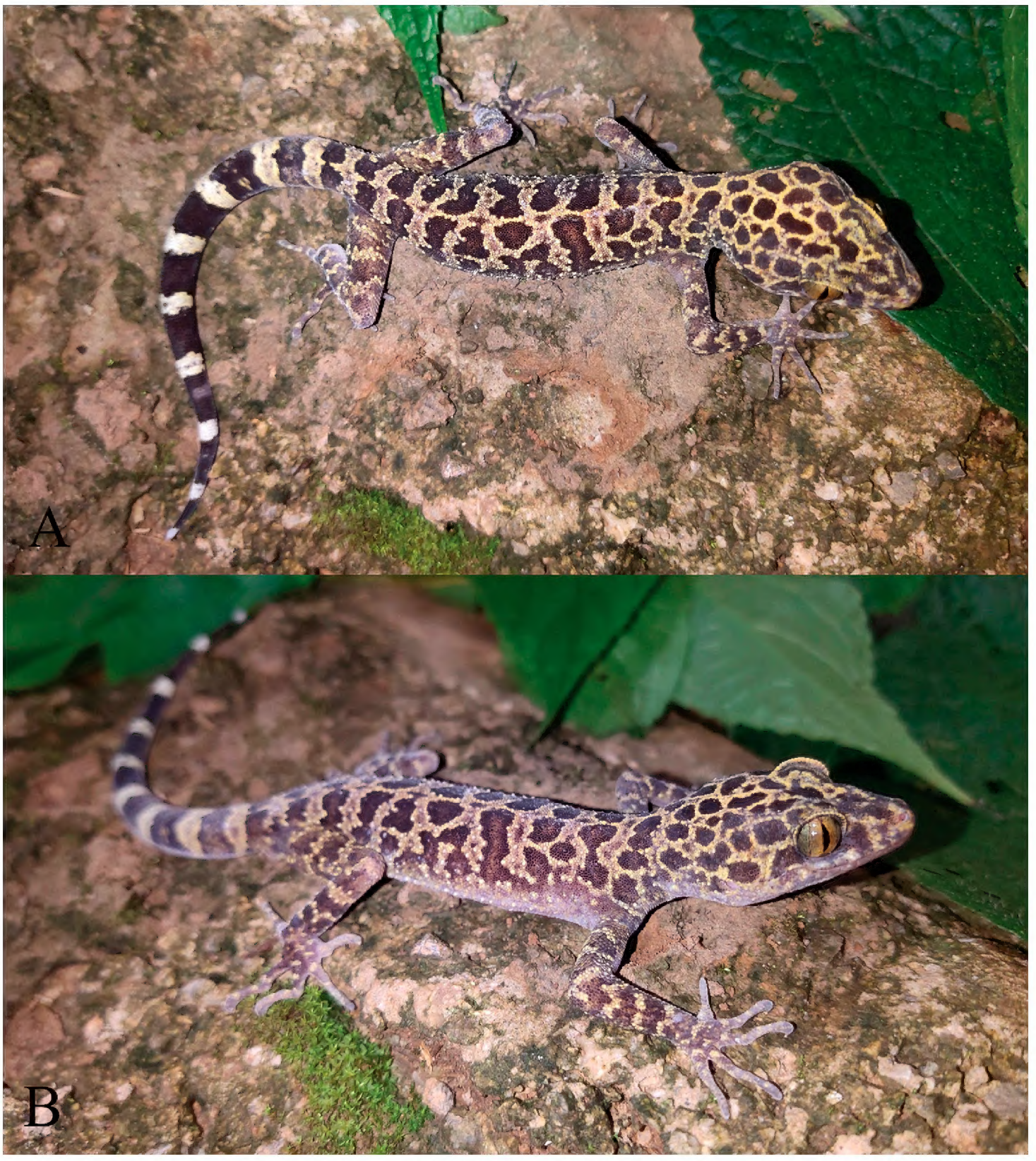

Figure 4. The holotype (KIZL20200049) of *Cyrtodactylus zhenkangensis* sp. nov. in life **A** dorsal view **B** lateral view.

or pitted femoral scales on the left side and nine poreless or pitted femoral scales on the right side; 5/5 femoral pores; 5/3 precloacal pores, separated by one poreless scale; most precloacal pores are positioned in the posterior margin of their scales and femoral pores positioned in the center of scales.

Fore and hind limbs moderately slender (ForeaL/SVL 0.17, SL/SVL 0.20); dorsal surface of forelimbs covered by a few weakly developed tubercles; interdigital webbing absent; lamellae under finger IV 20/18, under toe IV 21/23; relative length of fingers I<II<V<III <IV, relative length of toes I<II<III<V<IV.

Table 2. Measurements (mm) and meristic data for the type series of *Cyrtodactylus zhenkangensis* sp. nov. Abbreviations defined in Materials and methods.

	KIZL2020049 Holotype	KIZL2020046 Paratype	KIZL2020047 Paratype	KIZL2020048 Paratype	KIZL2020050 Paratype
Sex	Male	Subadult male	Subadult female	Female	Female
SVL	87.4	64.1	66.2	78.1	85.5
TaL	98.1	73.2	76.3	86.9	96.8
HH	11.5	9.0	8.5	10.3	10.4
HL	23.9	18.6	18.6	22.0	24.2
HW	18.8	13.9	14.2	17.1	17.8
OD	6.8	5.1	5.3	6.3	6.8
SE	9.7	7.9	8.0	9.3	9.9
EE	7.6	5.7	5.8	6.7	7.1
IND	3.1	2.5	2.6	3.0	3.2
IOD	8.3	5.8	6.1	7.2	7.7
ED	1.8	1.4	1.3	1.3	1.8
AG	35.5	25.7	25.4	33.2	36.1
ForeaL	15.2	11.5	11.6	13.1	14.5
SL	17.8	13.0	13.5	15.9	16.7
RW	4.1	3.3	3.2	3.7	4.2
RH	2.7	2.0	1.6	2.0	2.4
MW	3.4	3.1	2.7	3.2	3.8
ML	2.8	2.2	2.2	2.1	2.9
SPL	10/10	10/10	10/11	11/10	10/10
IFL	10/10	8/8	10/10	9/9	8/7
I	1	1	1	1	1
SC5SPL	37	32	34	28	33
PM	2	2	2	2	2
GSDT	9–10	9–10	8–9	8–10	8–9
DTR	24	23	21	20	22
PVT	29	27	32	33	28
V	33	32	32	34	33
EFS	13/15	14/14	14/13	13/12	14/15
PP	8	9 (pitted)	9 (pitted)	8 (pitted)	7 (pitted)
FP	5/5	2/2 (pitted)	1/0 (pitted)	3/0 (pitted)	2/2 (pitted)
PAT	2/3	2/2	2/2	3/3	2/3
LD4	20/18	19/20	19/18	21/20	21/19
LT4	21/23	23/22	22/22	22/21	22/22

Tail complete, longer than snout-vent length (TaL/SVL 1.12); 2/3 postcloacal tubercles; dorsal tail base with tubercles; subcaudals smooth, enlarged, arranged alternately in single and double series at anterior and mostly singly at middle and posterior parts.

Color of holotype in life. Head brown with pale-yellow, slightly symmetrical reticulations on either side of the midline, no dark-colored nuchal loop; dorsum of body brown with approximately nine pale-yellow, transverse, irregular bands from forelimb insertions to base of tail and one longitudinal, continuous, narrow vertebral stripe; dorsal surface of limbs brown with some light-yellow, irregularly shaped bands, some small, light-yellow spots on the dorsum of fingers and toes; ventral surface of head, body, and limbs grey with no stripes or spots; tail brownish black with ten yellowish white rings; iris copper-yellow.

Variations. Color pattern variations are shown in Figure 5, and morphometric and meristic differences are presented in Table 2. Morphologically the paratypes resemble

Figure 5. The paratypes of *Cyrtodactylus zhenkangensis* sp. nov. in life **A** subadult male (KIZL2020046) **B** subadult female (KIZL2020047) **C** adult female (KIZL2020048) **D** adult female (KIZL2020050).

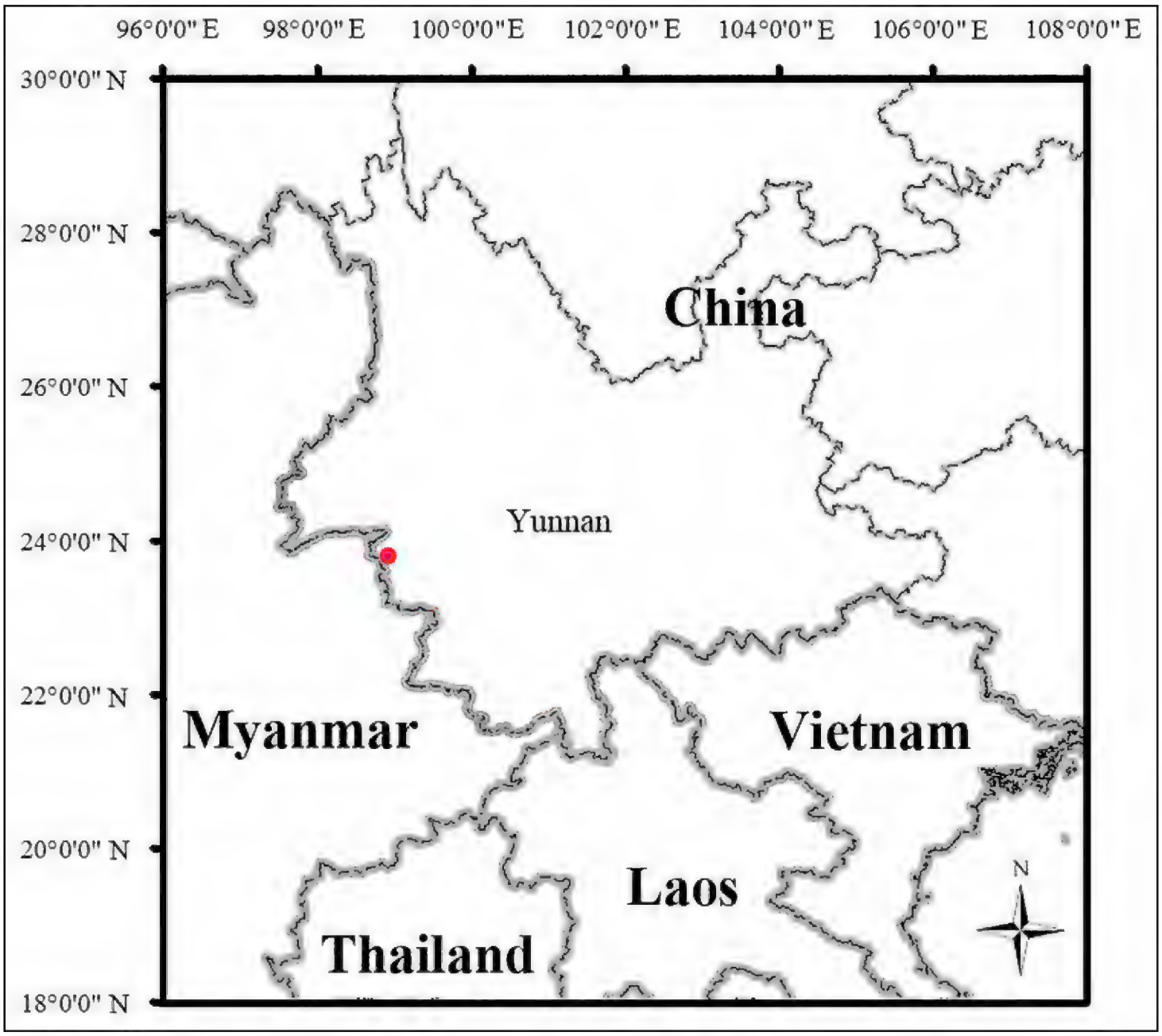

Figure 6. Map showing the type locality (red dot) of *Cyrtodactylus zhenkangensis* sp. nov. in Zhenkang County, Yunnan Province, China.

the holotype except as follows: KIZL2020046 and KIZL2020047 each has one vertebral stripe like the holotype but it is discontinuous; KIZL2020050 has one continuous vertebral strip and two discontinuous, longitudinal, narrow stripes on the sides of vertebral strip; KIZL2020048 only has transverse bands and no vertebra stripe. All paratypes have continuous precloacal pores (pitted) and fewer femoral pores (pitted).

Distribution. The new species is currently known only from the type locality in Zhenkang County, Yunnan Province, China.

Natural history. All specimens were found at night between 19:00 and 21:00 on limestone cliffs of the karst formations. The surrounding habitat was primary forest with a stream nearby. No eggs or juveniles were found.

Comparisons. *Cyrtodactylus zhenkangensis* sp. nov. is distinguishable from all other members of the *C. wayakonei* group by a unique combination of morphological characters. *Cyrtodactylus zhenkangensis* sp. nov. differs from *C. bichnganae* Ngo & Grismer, 2010;

Figure 7. Habitat of *Cyrtodactylus zhenkangensis* sp. nov. at the type locality in Zhenkang County, Yunnan Province, China.

C. huongsonensis Luu, Nguyen, Do & Ziegler, 2011; and *C. sonlaensis* Nguyen, Pham, Ziegler, Ngo & Le, 2017 in having fewer femoral pores in males (4–10 vs 15–29).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. bobrovi* Nguyen, Le, Pham, Ngo, Hoang, Pham & Ziegler, 2015; *C. otai* Nguyen, Le, Pham, Ngo, Hoang, Pham & Ziegler, 2015; and *C. vilaphongi* Schneider, Nguyen, Le, Nophaseud, Bonkowski & Ziegler, 2014 in having enlarged subcaudal scales (vs lacking enlarged subcaudals).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. chauquangensis* Hoang, Orlov, Ananjeva, Johns, Hoang & Dau, 2007; *C. cucphuongensis* Ngo & Chan, 2011; *C. houaphanensis* Schneider, Luu, Sitthivong, Teynié, Le, Nguyen & Ziegler, 2020; *C. puhuensis* Nguyen, Yang, Le, Nguyen, Orlov, Hoang, Nguyen, Jin, Rao, Hoang, Che, Murphy & Zhang, 2014; *C. spelaeus* Nazarov, Poyarkov, Orlov, Nguyen, Milto, Martynov, Konstantinov & Chulisov, 2014; and *C. taybacensis* Pham, Le, Ngo, Ziegler & Nguyen, 2019 in having femoral pores in males (vs lacking femoral pores in males).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. martini* in having femoral pores in males (vs lacking femoral pores in males) and more irregular transverse bands on the dorsum of body (8–9 vs 5–7).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. ngoiensis* Schneider, Luu, Sitthivong, Teynié, Le, Nguyen & Ziegler, 2020 and *C. soni* Le, Nguyen, Le & Ziegler, 2016 in its smaller body size (64.1–87.4 mm vs 62.9–103 mm) and having more lamellae under finger IV (18–21 vs 15–19) and toe IV (21–23 vs 18–22).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. wayakonei* in having enlarged subcaudal scales (vs lacking enlarged subcaudals) and with more irregular transverse bands on the dorsum of body (8–9 vs 5–7).

For other species which were not included in the phylogenetic analyses and resemble *Cyrtodactylus zhenkangensis* sp. nov. in morphology. *Cyrtodactylus zhenkangensis* sp. nov. differs from *C. auribalteatus* Sumontha, Panitvong & Deein, 2010 in having more transverse bands on the dorsum of body (8–9 vs 4–5), obvious reticulations on the dorsum of head (vs no obvious reticulations) and absent dark-colored nuchal loop (vs present).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. doisuthep* Kunya, Panmongkol, Pauwels, Sumontha, Meewasana, Bunkhwamdi & Dangsri, 2014 in having fewer femoral pores (0–10 vs 12–14), more precloacal pores (7–9 vs 6), and absent dark-colored nuchal loop (vs present).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. dumnuii* Bauer, Kunya, Sumontha, Niyomwan, Pauwels, Chanhome & Kunya, 2010 in having more lamellae under toe IV (21–23 vs 19), absent dark-colored nuchal loop (vs present), and obvious reticulations on the dorsum of head (vs not obvious or no reticulations).

Cyrtodactylus zhenkangensis sp. nov. differs from *C. erythrops* Bauer, Kunya, Sumontha, Niyomwan, Panitvong, Pauwels, Chanhome & Kunya, 2009 in having fewer femoral pores in males (4–10 vs 18–20), more lamellae under finger IV (18–21 vs 16) and toe IV (21–23 vs 20), and more transverse bands on the dorsum of body (8–9 vs 6–7).

Discussion

According to Pham et al. (2019) and Schneider et al. (2020), the *Cyrtodactylus wayakonei* species group contains 16 species, namely *C. bichnganae*, *C. bobrovi*, *C. chauquangensis*, *C. cucphuongensis*, *C. houaphanensis*, *C. huongsonensis*, *C. martini*, *C. ngoiensis*, *C. otai*, *C. puhuensis*, *C. soni*, *C. sonlaensis*, *C. spelaeus*, *C. taybacensis*, *C. vilaphongi*, and *C. wayakonei*. However, we speculate that there are still some other species (e.g., *C. auribalteatus*, *C. doisuthep*, *C. dumnuii*, and *C. erythrops*) which were not included in the phylogenetic analyses also belong to this species group based on morphology, molecular evidence is needed to clarify these problems.

Although the distribution of the new species is distant from the distributions of *C. martini* and *C. wayakonei*, the new species is most similar to the latter two in both morphology and phylogeny. The new species is not found in a protected area; the type locality is just beside the county seat, where there are human activities during the day but usually not at night. This species is nocturnal, so it may be less affected by human activities.

There are many other karst formations in Yunnan, some of which remain insufficiently surveyed. We are continuing to conduct more expeditions in these regions, and it is likely that additional new species of *Cyrtodactylus* will be found in these karst systems.

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